

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: St. Geme III, Joseph W.
Falkow, Stanley
- (ii) TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 - (B) STREET: 4 Embarcadero Center, Suite 3400
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 94111-4187
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/296,791
 - (B) FILING DATE: 25-AUG-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Trecartin, Richard F.
 - (B) REGISTRATION NUMBER: 31,801
 - (C) REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 781-1989
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 - (C) TELEX: 910 277299

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 60..4241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCAATAGTCG TTAACTAGT ATTTTTTAAT ACGAAAAATT ACTTAATTAA ATAAACATT      59
ATG AAA AAA ACT GTA TTT CGT CTT AAT TTT TTA ACC GCT TGC ATT TCA      107
Met Lys Lys Thr Val Phe Arg Leu Asn Phe Leu Thr Ala Cys Ile Ser
  1             5             10             15

TTA GGG ATA GTA TCG CAA GCG TGG GCT GGT CAC ACT TAT TTT GGG ATT      155

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Leu Gly Ile Val Ser Gln Ala Trp Ala Gly His Thr Tyr Phe Gly Ile	
20 25 30	
GAT TAC CAA TAT TAT CGT GAT TTT GCC GAG AAT AAA GGG AAG TTC ACA	203
Asp Tyr Gln Tyr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe Thr	
35 40 45	
GTT GGG GCT CAA AAT ATT AAG GTT TAT AAC AAA CAA GGG CAA TTA GTT	251
Val Gly Ala Gln Asn Ile Lys Val Tyr Asn Lys Gln Gly Gln Leu Val	
50 55 60	
GGC ACA TCA ATG ACA AAA GCC CCG ATG ATT GAT TTT TCT GTA GTG TCA	299
Gly Thr Ser Met Thr Lys Ala Pro Met Ile Asp Phe Ser Val Val Ser	
65 70 75 80	
CGT AAC GGC GTG GCA GCC TTG GTT GAA AAT CAA TAT ATT GTG AGC GTG	347
Arg Asn Gly Val Ala Ala Leu Val Glu Asn Gln Tyr Ile Val Ser Val	
85 90 95	
GCA CAT AAC GTA GGA TAT ACA GAT GTT GAT TTT GGT GCA GAG GGA AAC	395
Ala His Asn Val Gly Tyr Thr Asp Val Asp Phe Gly Ala Glu Gly Asn	
100 105 110	
AAC CCC GAT CAA CAT CGT TTT ACT TAT AAG ATT GTA AAA CGA AAT AAC	443
Asn Pro Asp Gln His Arg Phe Thr Tyr Lys Ile Val Lys Arg Asn Asn	
115 120 125	
TAC AAA AAA GAT AAT TTA CAT CCT TAT GAG GAC GAT TAC CAT AAT CCA	491
Tyr Lys Lys Asp Asn Leu His Pro Tyr Glu Asp Asp Tyr His Asn Pro	
130 135 140	
CGA TTA CAT AAA TTC GTT ACA GAA GCG GCT CCA ATT GAT ATG ACT TCG	539
Arg Leu His Lys Phe Val Thr Glu Ala Ala Pro Ile Asp Met Thr Ser	
145 150 155 160	
AAT ATG AAT GGC AGT ACT TAT TCA GAT AGA ACA AAA TAT CCA GAA CGT	587
Asn Met Asn Gly Ser Thr Tyr Ser Asp Arg Thr Lys Tyr Pro Glu Arg	
165 170 175	
GTT CGT ATC GGC TCT GGA CGG CAG TTT TGG CGA AAT GAT CAA GAC AAA	635
Val Arg Ile Gly Ser Gly Arg Gln Phe Trp Arg Asn Asp Gln Asp Lys	
180 185 190	
GGC GAC CAA GTT GCC GGT GCA TAT CAT TAT CTG ACA GCT GGC AAT ACA	683
Gly Asp Gln Val Ala Gly Ala Tyr His Tyr Leu Thr Ala Gly Asn Thr	
195 200 205	
CAC AAT CAG CGT GGA GCA GGT AAT GGA TAT TCG TAT TTG GGA GGC GAT	731
His Asn Gln Arg Gly Ala Gly Asn Gly Tyr Ser Tyr Leu Gly Gly Asp	
210 215 220	
GTT CGT AAA GCG GGA GAA TAT GGT CCA TTA CCG ATT GCA GGC TCA AAG	779
Val Arg Lys Ala Gly Glu Tyr Gly Pro Leu Pro Ile Ala Gly Ser Lys	
225 230 235 240	
GGG GAC AGT GGT TCT CCG ATG TTT ATT TAT GAT GCT GAA AAA CAA AAA	827
Gly Asp Ser Gly Ser Pro Met Phe Ile Tyr Asp Ala Glu Lys Gln Lys	
245 250 255	
TGG TTA ATT AAT GGG ATA TTA CGG GAA GGC AAC CCT TTT GAA GGC AAA	875
Trp Leu Ile Asn Gly Ile Leu Arg Glu Gly Asn Pro Phe Glu Gly Lys	
260 265 270	
GAA AAT GGG TTT CAA TTG GTT CGC AAA TCT TAT TTT GAT GAA ATT TTC	923
Glu Asn Gly Phe Gln Leu Val Arg Lys Ser Tyr Phe Asp Glu Ile Phe	

275	280	285	
GAA AGA GAT TTA CAT ACA TCA CTT TAC ACC CGA GCT GGT AAT GGA GTG			971
Glu Arg Asp Leu His Thr Ser Leu Tyr Thr Arg Ala Gly Asn Gly Val			
290	295	300	
TAC ACA ATT AGT GGA AAT GAT AAT GGT CAG GGG TCT ATA ACT CAG AAA			1019
Tyr Thr Ile Ser Gly Asn Asp Asn Gly Gln Gly Ser Ile Thr Gln Lys			
305	310	315	320
TCA GGA ATA CCA TCA GAA ATT AAA ATT ACG TTA GCA AAT ATG AGT TTA			1067
Ser Gly Ile Pro Ser Glu Ile Lys Ile Thr Leu Ala Asn Met Ser Leu			
325	330	335	
CCT TTG AAA GAG AAG GAT AAA GTT CAT AAT CCT AGA TAT GAC GGA CCT			1115
Pro Leu Lys Glu Lys Asp Lys Val His Asn Pro Arg Tyr Asp Gly Pro			
340	345	350	
AAT ATT TAT TCT CCA CGT TTA AAC AAT GGA GAA ACG CTA TAT TTT ATG			1163
Asn Ile Tyr Ser Pro Arg Leu Asn Asn Gly Glu Thr Leu Tyr Phe Met			
355	360	365	
GAT CAA AAA CAA GGA TCA TTA ATC TTC GCA TCT GAC ATT AAC CAA GGG			1211
Asp Gln Lys Gln Gly Ser Leu Ile Phe Ala Ser Asp Ile Asn Gln Gly			
370	375	380	
GCG GGT GGT CTT TAT TTT GAG GGT AAT TTT ACA GTA TCT CCA AAT TCT			1259
Ala Gly Gly Leu Tyr Phe Glu Gly Asn Phe Thr Val Ser Pro Asn Ser			
385	390	395	400
AAC CAA ACT TGG CAA GGA GCT GGC ATA CAT GTA AGT GAA AAT AGC ACC			1307
Asn Gln Thr Trp Gln Gly Ala Gly Ile His Val Ser Glu Asn Ser Thr			
405	410	415	
GTT ACT TGG AAA GTA AAT GGC GTG GAA CAT GAT CGA CTT TCT AAA ATT			1355
Val Thr Trp Lys Val Asn Gly Val Glu His Asp Arg Leu Ser Lys Ile			
420	425	430	
GGT AAA GGA ACA TTG CAC GTT CAA GCC AAA GGG GAA AAT AAA GGT TCG			1403
Gly Lys Gly Thr Leu His Val Gln Ala Lys Gly Glu Asn Lys Gly Ser			
435	440	445	
ATC AGC GTA GGC GAT GGT AAA GTC ATT TTG GAG CAG CAG GCA GAC GAT			1451
Ile Ser Val Gly Asp Gly Lys Val Ile Leu Glu Gln Gln Ala Asp Asp			
450	455	460	
CAA GGC AAC AAA CAA GCC TTT AGT GAA ATT GGC TTG GTT AGC GGC AGA			1499
Gln Gly Asn Lys Gln Ala Phe Ser Glu Ile Gly Leu Val Ser Gly Arg			
465	470	475	480
GGG ACT GTT CAA TTA AAC GAT GAT AAA CAA TTT GAT ACC GAT AAA TTT			1547
Gly Thr Val Gln Leu Asn Asp Asp Lys Phe Asp Thr Asp Lys Phe			
485	490	495	
TAT TTC GGC TTT CGT GGT GGT CGC TTA GAT CTT AAC GGG CAT TCA TTA			1595
Tyr Phe Gly Phe Arg Gly Gly Arg Leu Asp Leu Asn Gly His Ser Leu			
500	505	510	
ACC TTT AAA CGT ATC CAA AAT ACG GAC GAG GGG GCA ATG ATT GTG AAC			1643
Thr Phe Lys Arg Ile Gln Asn Thr Asp Glu Gly Ala Met Ile Val Asn			
515	520	525	
CAT AAT ACA ACT CAA GCC GCT AAT GTC ACT ATT ACT GGG AAC GAA AGC			1691
His Asn Thr Thr Gln Ala Ala Asn Val Thr Ile Thr Gly Asn Glu Ser			
530	535	540	

ATT GTT CTA CCT AAT GGA AAT AAT ATT AAT AAA CTT GAT TAC AGA AAA	1739
Ile Val Leu Pro Asn Gly Asn Asn Ile Asn Lys Leu Asp Tyr Arg Lys	
545 550 555 560	
GAA ATT GCC TAC AAC GGT TGG TTT GGC GAA ACA GAT AAA AAT AAA CAC	1787
Glu Ile Ala Tyr Asn Gly Trp Phe Gly Glu Thr Asp Lys Asn Lys His	
565 570 575	
AAT GGG CGA TTA AAC CTT ATT TAT AAA CCA ACC ACA GAA GAT CGT ACT	1835
Asn Gly Arg Leu Asn Leu Ile Tyr Lys Pro Thr Thr Glu Asp Arg Thr	
580 585 590	
TTG CTA CTT TCA GGT GGT ACA AAT TTA AAA GGC GAT ATT ACC CAA ACA	1883
Leu Leu Leu Ser Gly Gly Thr Asn Leu Lys Gly Asp Ile Thr Gln Thr	
595 600 605	
AAA GGT AAA CTA TTT TTC AGC GGT AGA CCG ACA CCG CAC GCC TAC AAT	1931
Lys Gly Lys Leu Phe Phe Ser Gly Arg Pro Thr Pro His Ala Tyr Asn	
610 615 620	
CAT TTA AAT AAA CGT TGG TCA GAA ATG GAA GGT ATA CCA CAA GGC GAA	1979
His Leu Asn Lys Arg Trp Ser Glu Met Glu Gly Ile Pro Gln Gly Glu	
625 630 635 640	
ATT GTG TGG GAT CAC GAT TGG ATC AAC CGT ACA TTT AAA GCT GAA AAC	2027
Ile Val Trp Asp His Asp Trp Ile Asn Arg Thr Phe Lys Ala Glu Asn	
645 650 655	
TTC CAA ATT AAA GGC GGA AGT GCG GTG GTT TCT CGC AAT GTT TCT TCA	2075
Phe Gln Ile Lys Gly Gly Ser Ala Val Val Ser Arg Asn Val Ser Ser	
660 665 670	
ATT GAG GGA AAT TGG ACA GTC AGC AAT AAT GCA AAT GCC ACA TTT GGT	2123
Ile Glu Gly Asn Trp Thr Val Ser Asn Asn Ala Asn Ala Thr Phe Gly	
675 680 685	
GTT GTG CCA AAT CAA CAA AAT ACC ATT TGC ACG CGT TCA GAT TGG ACA	2171
Val Val Pro Asn Gln Gln Asn Thr Ile Cys Thr Arg Ser Asp Trp Thr	
690 695 700	
GGA TTA ACG ACT TGT CAA AAA GTG GAT TTA ACC GAT ACA AAA GTT ATT	2219
Gly Leu Thr Thr Cys Gln Lys Val Asp Leu Thr Asp Thr Lys Val Ile	
705 710 715 720	
AAT TCT ATA CCA AAA ACA CAA ATC AAT GGC TCT ATT AAT TTA ACT GAT	2267
Asn Ser Ile Pro Lys Thr Gln Ile Asn Gly Ser Ile Asn Leu Thr Asp	
725 730 735	
AAT GCA ACG GCG AAT GTT AAA GGT TTA GCA AAA CTT AAT GGC AAT GTC	2315
Asn Ala Thr Ala Asn Val Lys Gly Leu Ala Lys Leu Asn Gly Asn Val	
740 745 750	
ACT TTA ACA AAT CAC AGC CAA TTT ACA TTA AGC AAC AAT GCC ACC CAA	2363
Thr Leu Thr Asn His Ser Gln Phe Thr Leu Ser Asn Asn Ala Thr Gln	
755 760 765	
ATA GGC AAT ATT CGA CTT TCC GAC AAT TCA ACT GCA ACG GTG GAT AAT	2411
Ile Gly Asn Ile Arg Leu Ser Asp Asn Ser Thr Ala Thr Val Asp Asn	
770 775 780	
GCA AAC TTG AAC GGT AAT GTG CAT TTA ACG GAT TCA GCT CAA TTT TCT	2459
Ala Asn Leu Asn Gly Asn Val His Leu Thr Asp Ser Ala Gln Phe Ser	
785 790 795 800	
TTA AAA AAC AGC CAT TTT TCG CAC CAA ATT CAG GGA GAC AAA GGC ACA	2507

Leu Lys Asn Ser His Phe Ser His Gln Ile Gln Gly Asp Lys Gly Thr
 805 810 815

ACA GTG ACG TTG GAA AAT GCG ACT TGG ACA ATG CCT AGC GAT ACT ACA 2555
 Thr Val Thr Leu Glu Asn Ala Thr Trp Thr Met Pro Ser Asp Thr Thr
 820 825 830

TTG CAG AAT TTA ACG CTA AAT AAC AGT ACG ATC ACG TTA AAT TCA GCT 2603
 Leu Gln Asn Leu Thr Leu Asn Asn Ser Thr Ile Thr Leu Asn Ser Ala
 835 840 845

TAT TCA GCT AGC TCA AAC AAT ACG CCA CGT CGC CGT TCA TTA GAG ACG 2651
 Tyr Ser Ala Ser Ser Asn Asn Thr Pro Arg Arg Arg Ser Leu Glu Thr
 850 855 860

GAA ACA ACG CCA ACA TCG GCA GAA CAT CGT TTC AAC ACA TTG ACA GTA 2699
 Glu Thr Thr Pro Thr Ser Ala Glu His Arg Phe Asn Thr Leu Thr Val
 865 870 875 880

AAT GGT AAA TTG AGT GGG CAA GGC ACA TTC CAA TTT ACT TCA TCT TTA 2747
 Asn Gly Lys Leu Ser Gly Gln Gly Thr Phe Gln Phe Thr Ser Ser Leu
 885 890 895

TTT GGC TAT AAA AGC GAT AAA TTA AAA TTA TCC AAT GAC GCT GAG GGC 2795
 Phe Gly Tyr Lys Ser Asp Lys Leu Lys Leu Ser Asn Asp Ala Glu Gly
 900 905 910

GAT TAC ATA TTA TCT GTT CGC AAC ACA GGC AAA GAA CCC GAA ACC CTT 2843
 Asp Tyr Ile Leu Ser Val Arg Asn Thr Gly Lys Glu Pro Glu Thr Leu
 915 920 925

GAG CAA TTA ACT TTG GTT GAA AGC AAA GAT AAT CAA CCG TTA TCA GAT 2891
 Glu Gln Leu Thr Leu Val Glu Ser Lys Asp Asn Gln Pro Leu Ser Asp
 930 935 940

AAG CTC AAA TTT ACT TTA GAA AAT GAC CAC GTT GAT GCA GGT GCA TTA 2939
 Lys Leu Lys Phe Thr Leu Glu Asn Asp His Val Asp Ala Gly Ala Leu
 945 950 955 960

CGT TAT AAA TTA GTG AAG AAT GAT GGC GAA TTC CGC TTG CAT AAC CCA 2987
 Arg Tyr Lys Leu Val Lys Asn Asp Gly Glu Phe Arg Leu His Asn Pro
 965 970 975

ATA AAA GAG CAG GAA TTG CAC AAT GAT TTA GTA AGA GCA GAG CAA GCA 3035
 Ile Lys Glu Gln Glu Leu His Asn Asp Leu Val Arg Ala Glu Gln Ala
 980 985 990

GAA CGA ACA TTA GAA GCC AAA CAA GTT GAA CCG ACT GCT AAA ACA CAA 3083
 Glu Arg Thr Leu Glu Ala Lys Gln Val Glu Pro Thr Ala Lys Thr Gln
 995 1000 1005

ACA GGT GAG CCA AAA GTG CGG TCA AGA AGA GCA GCG AGA GCA GCG TTT 3131
 Thr Gly Glu Pro Lys Val Arg Ser Arg Arg Ala Ala Arg Ala Ala Phe
 1010 1015 1020

CCT GAT ACC CTG CCT GAT CAA AGC CTG TTA AAC GCA TTA GAA GCC AAA 3179
 Pro Asp Thr Leu Pro Asp Gln Ser Leu Leu Asn Ala Leu Glu Ala Lys
 1025 1030 1035 1040

CAA GCT GAA CTG ACT GCT GAA ACA CAA AAA AGT AAG GCA AAA ACA AAA 3227
 Gln Ala Glu Leu Thr Ala Glu Thr Gln Lys Ser Lys Ala Lys Thr Lys
 1045 1050 1055

AAA GTG CGG TCA AAA AGA GCA GTG TTT TCT GAT CCC CTG CTT GAT CAA 3275
 Lys Val Arg Ser Lys Arg Ala Val Phe Ser Asp Pro Leu Leu Asp Gln

1060	1065	1070	
AGC CTG TTC GCA TTA GAA GCC GCA CTT GAG GTT ATT GAT GCC CCA CAG			3323
Ser Leu Phe Ala Leu Glu Ala Ala Leu Glu Val Ile Asp Ala Pro Gln			
1075	1080	1085	
CAA TCG GAA AAA GAT CGT CTA GCT CAA GAA GAA GCG GAA AAA CAA CGC			3371
Gln Ser Glu Lys Asp Arg Leu Ala Gln Glu Ala Glu Lys Gln Arg			
1090	1095	1100	
AAA CAA AAA GAC TTG ATC AGC CGT TAT TCA AAT AGT GCG TTA TCA GAA			3419
Lys Gln Lys Asp Leu Ile Ser Arg Tyr Ser Asn Ser Ala Leu Ser Glu			
1105	1110	1115	1120
TTA TCT GCA ACA GTA AAT AGT ATG CTT TCT GTT CAA GAT GAA TTA GAT			3467
Leu Ser Ala Thr Val Asn Ser Met Leu Ser Val Gln Asp Glu Leu Asp			
1125	1130	1135	
CGT CTT TTT GTA GAT CAA GCA CAA TCT GCC GTG TGG ACA AAT ATC GCA			3515
Arg Leu Phe Val Asp Gln Ala Gln Ser Ala Val Trp Thr Asn Ile Ala			
1140	1145	1150	
CAG GAT AAA AGA CGC TAT GAT TCT GAT GCG TTC CGT GCT TAT CAG CAG			3563
Gln Asp Lys Arg Arg Tyr Asp Ser Asp Ala Phe Arg Ala Tyr Gln Gln			
1155	1160	1165	
CAG AAA ACG AAC TTA CGT CAA ATT GGG GTG CAA AAA GCC TTA GCT AAT			3611
Gln Lys Thr Asn Leu Arg Gln Ile Gly Val Gln Lys Ala Leu Ala Asn			
1170	1175	1180	
GGA CGA ATT GGG GCA GTT TTC TCG CAT AGC CGT TCA GAT AAT ACC TTT			3659
Gly Arg Ile Gly Ala Val Phe Ser His Ser Arg Ser Asp Asn Thr Phe			
1185	1190	1195	1200
GAT GAA CAG GTT AAA AAT CAC GCG ACA TTA ACG ATG ATG TCG GGT TTT			3707
Asp Glu Gln Val Lys Asn His Ala Thr Leu Thr Met Met Ser Gly Phe			
1205	1210	1215	
GCC CAA TAT CAA TGG GGC GAT TTA CAA TTT GGT GTA AAC GTG GGA ACG			3755
Ala Gln Tyr Gln Trp Gly Asp Leu Gln Phe Gly Val Asn Val Gly Thr			
1220	1225	1230	
GGA ATC AGT GCG AGT AAA ATG GCT GAA GAA CAA AGC CGA AAA ATT CAT			3803
Gly Ile Ser Ala Ser Lys Met Ala Glu Glu Gln Ser Arg Lys Ile His			
1235	1240	1245	
CGA AAA GCG ATA AAT TAT GGC GTG AAT GCA AGT TAT CAG TTC CGT TTA			3851
Arg Lys Ala Ile Asn Tyr Gly Val Asn Ala Ser Tyr Gln Phe Arg Leu			
1250	1255	1260	
GGG CAA TTG GGC ATT CAG CCT TAT TTT GGA GTT AAT CGC TAT TTT ATT			3899
Gly Gln Leu Gly Ile Gln Pro Tyr Phe Gly Val Asn Arg Tyr Phe Ile			
1265	1270	1275	1280
GAA CGT GAA AAT TAT CAA TCT GAG GAA GTG AGA GTG AAA ACG CCT AGC			3947
Glu Arg Glu Asn Tyr Gln Ser Glu Glu Val Arg Val Lys Thr Pro Ser			
1285	1290	1295	
CTT GCA TTT AAT CGC TAT AAT GCT GGC ATT CGA GTT GAT TAT ACA TTT			3995
Leu Ala Phe Asn Arg Tyr Asn Ala Gly Ile Arg Val Asp Tyr Thr Phe			
1300	1305	1310	
ACT CCG ACA GAT AAT ATC AGC GTT AAG CCT TAT TTC TTC GTC AAT TAT			4043
Thr Pro Thr Asp Asn Ile Ser Val Lys Pro Tyr Phe Phe Val Asn Tyr			
1315	1320	1325	

GTT GAT GTT TCA AAC GCT AAC GTA CAA ACC ACG GTA AAT CTC ACG GTG 4091
 Val Asp Val Ser Asn Ala Asn Val Gln Thr Thr Val Asn Leu Thr Val
 1330 1335 1340
 TTG CAA CAA CCA TTT GGA CGT TAT TGG CAA AAA GAA GTG GGA TTA AAG 4139
 Leu Gln Gln Pro Phe Gly Arg Tyr Trp Gln Lys Glu Val Gly Leu Lys
 1345 1350 1355 1360
 GCA GAA ATT TTA CAT TTC CAA ATT TCC GCT TTT ATC TCA AAA TCT CAA 4187
 Ala Glu Ile Leu His Phe Gln Ile Ser Ala Phe Ile Ser Lys Ser Gln
 1365 1370 1375
 GGT TCA CAA CTC GGC AAA CAG CAA AAT GTG GGC GTG AAA TTG GGC TAT 4235
 Gly Ser Gln Leu Gly Lys Gln Gln Asn Val Gly Val Lys Leu Gly Tyr
 1380 1385 1390
 CGT TGG TAAAAATCA ACATAATTTT ATCGTTTATT GATAACAAG GTGGGTCAGA 4290
 Arg Trp
 TCAGATCCCA CCTTTTTTAT TCCAATAAT 4319

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1394 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Lys Thr Val Phe Arg Leu Asn Phe Leu Thr Ala Cys Ile Ser
 1 5 10 15
 Leu Gly Ile Val Ser Gln Ala Trp Ala Gly His Thr Tyr Phe Gly Ile
 20 25 30
 Asp Tyr Gln Tyr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe Thr
 35 40 45
 Val Gly Ala Gln Asn Ile Lys Val Tyr Asn Lys Gln Gly Gln Leu Val
 50 55 60
 Gly Thr Ser Met Thr Lys Ala Pro Met Ile Asp Phe Ser Val Val Ser
 65 70 75 80
 Arg Asn Gly Val Ala Ala Leu Val Glu Asn Gln Tyr Ile Val Ser Val
 85 90 95
 Ala His Asn Val Gly Tyr Thr Asp Val Asp Phe Gly Ala Glu Gly Asn
 100 105 110
 Asn Pro Asp Gln His Arg Phe Thr Tyr Lys Ile Val Lys Arg Asn Asn
 115 120 125
 Tyr Lys Lys Asp Asn Leu His Pro Tyr Glu Asp Asp Tyr His Asn Pro
 130 135 140
 Arg Leu His Lys Phe Val Thr Glu Ala Ala Pro Ile Asp Met Thr Ser
 145 150 155 160
 Asn Met Asn Gly Ser Thr Tyr Ser Asp Arg Thr Lys Tyr Pro Glu Arg
 165 170 175

Val Arg Ile Gly Ser Gly Arg Gln Phe Trp Arg Asn Asp Gln Asp Lys
180 185 190
Gly Asp Gln Val Ala Gly Ala Tyr His Tyr Leu Thr Ala Gly Asn Thr
195 200 205
His Asn Gln Arg Gly Ala Gly Asn Gly Tyr Ser Tyr Leu Gly Gly Asp
210 215 220
Val Arg Lys Ala Gly Glu Tyr Gly Pro Leu Pro Ile Ala Gly Ser Lys
225 230 235 240
Gly Asp Ser Gly Ser Pro Met Phe Ile Tyr Asp Ala Glu Lys Gln Lys
245 250 255
Trp Leu Ile Asn Gly Ile Leu Arg Glu Gly Asn Pro Phe Glu Gly Lys
260 265 270
Glu Asn Gly Phe Gln Leu Val Arg Lys Ser Tyr Phe Asp Glu Ile Phe
275 280 285
Glu Arg Asp Leu His Thr Ser Leu Tyr Thr Arg Ala Gly Asn Gly Val
290 295 300
Tyr Thr Ile Ser Gly Asn Asp Asn Gly Gln Gly Ser Ile Thr Gln Lys
305 310 315 320
Ser Gly Ile Pro Ser Glu Ile Lys Ile Thr Leu Ala Asn Met Ser Leu
325 330 335
Pro Leu Lys Glu Lys Asp Lys Val His Asn Pro Arg Tyr Asp Gly Pro
340 345 350
Asn Ile Tyr Ser Pro Arg Leu Asn Asn Gly Glu Thr Leu Tyr Phe Met
355 360 365
Asp Gln Lys Gln Gly Ser Leu Ile Phe Ala Ser Asp Ile Asn Gln Gly
370 375 380
Ala Gly Gly Leu Tyr Phe Glu Gly Asn Phe Thr Val Ser Pro Asn Ser
385 390 395 400
Asn Gln Thr Trp Gln Gly Ala Gly Ile His Val Ser Glu Asn Ser Thr
405 410 415
Val Thr Trp Lys Val Asn Gly Val Glu His Asp Arg Leu Ser Lys Ile
420 425 430
Gly Lys Gly Thr Leu His Val Gln Ala Lys Gly Glu Asn Lys Gly Ser
435 440 445
Ile Ser Val Gly Asp Gly Lys Val Ile Leu Glu Gln Gln Ala Asp Asp
450 455 460
Gln Gly Asn Lys Gln Ala Phe Ser Glu Ile Gly Leu Val Ser Gly Arg
465 470 475 480
Gly Thr Val Gln Leu Asn Asp Asp Lys Gln Phe Asp Thr Asp Lys Phe
485 490 495
Tyr Phe Gly Phe Arg Gly Gly Arg Leu Asp Leu Asn Gly His Ser Leu
500 505 510
Thr Phe Lys Arg Ile Gln Asn Thr Asp Glu Gly Ala Met Ile Val Asn
515 520 525
His Asn Thr Thr Gln Ala Ala Asn Val Thr Ile Thr Gly Asn Glu Ser

530					535					540					
Ile 545	Val	Leu	Pro	Asn	Gly 550	Asn	Asn	Ile	Asn	Lys 555	Leu	Asp	Tyr	Arg	Lys 560
Glu	Ile	Ala	Tyr	Asn 565	Gly	Trp	Phe	Gly	Glu 570	Thr	Asp	Lys	Asn	Lys 575	His
Asn	Gly	Arg	Leu 580	Asn	Leu	Ile	Tyr	Lys 585	Pro	Thr	Thr	Glu	Asp 590	Arg	Thr
Leu	Leu	Leu 595	Ser	Gly	Gly	Thr	Asn 600	Leu	Lys	Gly	Asp	Ile 605	Thr	Gln	Thr
Lys	Gly 610	Lys	Leu	Phe	Phe	Ser 615	Gly	Arg	Pro	Thr	Pro 620	His	Ala	Tyr	Asn
His 625	Leu	Asn	Lys	Arg	Trp 630	Ser	Glu	Met	Glu	Gly 635	Ile	Pro	Gln	Gly	Glu 640
Ile	Val	Trp	Asp	His 645	Asp	Trp	Ile	Asn	Arg 650	Thr	Phe	Lys	Ala	Glu 655	Asn
Phe	Gln	Ile	Lys 660	Gly	Gly	Ser	Ala	Val 665	Val	Ser	Arg	Asn	Val 670	Ser	Ser
Ile	Glu	Gly 675	Asn	Trp	Thr	Val	Ser 680	Asn	Asn	Ala	Asn 685	Ala	Thr	Phe	Gly
Val	Val 690	Pro	Asn	Gln	Gln	Asn 695	Thr	Ile	Cys	Thr	Arg 700	Ser	Asp	Trp	Thr
Gly 705	Leu	Thr	Thr	Cys	Gln 710	Lys	Val	Asp	Leu	Thr 715	Asp	Thr	Lys	Val	Ile 720
Asn	Ser	Ile	Pro	Lys 725	Thr	Gln	Ile	Asn	Gly 730	Ser	Ile	Asn	Leu	Thr 735	Asp
Asn	Ala	Thr	Ala 740	Asn	Val	Lys	Gly	Leu 745	Ala	Lys	Leu	Asn	Gly 750	Asn	Val
Thr	Leu	Thr 755	Asn	His	Ser	Gln	Phe 760	Thr	Leu	Ser	Asn 765	Asn	Ala	Thr	Gln
Ile	Gly 770	Asn	Ile	Arg	Leu	Ser 775	Asp	Asn	Ser	Thr	Ala 780	Thr	Val	Asp	Asn
Ala 785	Asn	Leu	Asn	Gly	Asn 790	Val	His	Leu	Thr	Asp 795	Ser	Ala	Gln	Phe	Ser 800
Leu	Lys	Asn	Ser	His 805	Phe	Ser	His	Gln	Ile 810	Gln	Gly	Asp	Lys	Gly 815	Thr
Thr	Val	Thr	Leu 820	Glu	Asn	Ala	Thr	Trp 825	Thr	Met	Pro	Ser	Asp 830	Thr	Thr
Leu	Gln	Asn 835	Leu	Thr	Leu	Asn	Asn 840	Ser	Thr	Ile	Thr	Leu	Asn 845	Ser	Ala
Tyr	Ser 850	Ala	Ser	Ser	Asn	Asn 855	Thr	Pro	Arg	Arg	Arg 860	Ser	Leu	Glu	Thr
Glu 865	Thr	Thr	Pro	Thr	Ser	Ala	Glu	His	Arg	Phe 875	Asn	Thr	Leu	Thr	Val 880
Asn	Gly	Lys	Leu	Ser 885	Gly	Gln	Gly	Thr	Phe 890	Gln	Phe	Thr	Ser	Ser 895	Leu

Phe Gly Tyr Lys Ser Asp Lys Leu Lys Leu Ser Asn Asp Ala Glu Gly
900 905 910
Asp Tyr Ile Leu Ser Val Arg Asn Thr Gly Lys Glu Pro Glu Thr Leu
915 920 925
Glu Gln Leu Thr Leu Val Glu Ser Lys Asp Asn Gln Pro Leu Ser Asp
930 935 940
Lys Leu Lys Phe Thr Leu Glu Asn Asp His Val Asp Ala Gly Ala Leu
945 950 955 960
Arg Tyr Lys Leu Val Lys Asn Asp Gly Glu Phe Arg Leu His Asn Pro
965 970 975
Ile Lys Glu Gln Glu Leu His Asn Asp Leu Val Arg Ala Glu Gln Ala
980 985 990
Glu Arg Thr Leu Glu Ala Lys Gln Val Glu Pro Thr Ala Lys Thr Gln
995 1000 1005
Thr Gly Glu Pro Lys Val Arg Ser Arg Arg Ala Ala Arg Ala Ala Phe
1010 1015 1020
Pro Asp Thr Leu Pro Asp Gln Ser Leu Leu Asn Ala Leu Glu Ala Lys
1025 1030 1035 1040
Gln Ala Glu Leu Thr Ala Glu Thr Gln Lys Ser Lys Ala Lys Thr Lys
1045 1050 1055
Lys Val Arg Ser Lys Arg Ala Val Phe Ser Asp Pro Leu Leu Asp Gln
1060 1065 1070
Ser Leu Phe Ala Leu Glu Ala Ala Leu Glu Val Ile Asp Ala Pro Gln
1075 1080 1085
Gln Ser Glu Lys Asp Arg Leu Ala Gln Glu Glu Ala Glu Lys Gln Arg
1090 1095 1100
Lys Gln Lys Asp Leu Ile Ser Arg Tyr Ser Asn Ser Ala Leu Ser Glu
1105 1110 1115 1120
Leu Ser Ala Thr Val Asn Ser Met Leu Ser Val Gln Asp Glu Leu Asp
1125 1130 1135
Arg Leu Phe Val Asp Gln Ala Gln Ser Ala Val Trp Thr Asn Ile Ala
1140 1145 1150
Gln Asp Lys Arg Arg Tyr Asp Ser Asp Ala Phe Arg Ala Tyr Gln Gln
1155 1160 1165
Gln Lys Thr Asn Leu Arg Gln Ile Gly Val Gln Lys Ala Leu Ala Asn
1170 1175 1180
Gly Arg Ile Gly Ala Val Phe Ser His Ser Arg Ser Asp Asn Thr Phe
1185 1190 1195 1200
Asp Glu Gln Val Lys Asn His Ala Thr Leu Thr Met Met Ser Gly Phe
1205 1210 1215
Ala Gln Tyr Gln Trp Gly Asp Leu Gln Phe Gly Val Asn Val Gly Thr
1220 1225 1230
Gly Ile Ser Ala Ser Lys Met Ala Glu Glu Gln Ser Arg Lys Ile His
1235 1240 1245
Arg Lys Ala Ile Asn Tyr Gly Val Asn Ala Ser Tyr Gln Phe Arg Leu

1250	1255	1260
Gly Gln Leu Gly Ile Gln Pro Tyr Phe Gly Val Asn Arg Tyr Phe Ile		
1265	1270	1275 1280
Glu Arg Glu Asn Tyr Gln Ser Glu Glu Val Arg Val Lys Thr Pro Ser		
	1285	1290 1295
Leu Ala Phe Asn Arg Tyr Asn Ala Gly Ile Arg Val Asp Tyr Thr Phe		
	1300	1305 1310
Thr Pro Thr Asp Asn Ile Ser Val Lys Pro Tyr Phe Phe Val Asn Tyr		
	1315	1320 1325
Val Asp Val Ser Asn Ala Asn Val Gln Thr Thr Val Asn Leu Thr Val		
	1330	1335 1340
Leu Gln Gln Pro Phe Gly Arg Tyr Trp Gln Lys Glu Val Gly Leu Lys		
1345	1350	1355 1360
Ala Glu Ile Leu His Phe Gln Ile Ser Ala Phe Ile Ser Lys Ser Gln		
	1365	1370 1375
Gly Ser Gln Leu Gly Lys Gln Gln Asn Val Gly Val Lys Leu Gly Tyr		
	1380	1385 1390
Arg Trp		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	Asn	Lys	Lys	Phe	Lys	Leu	Asn	Phe	Ile	Ala	Leu	Thr	Val	Ala
1				5					10					15	
Tyr	Ala	Leu	Thr	Pro	Tyr	Thr	Glu	Ala	Ala	Leu	Val	Arg	Asp	Asp	Val
			20					25					30		
Asp	Tyr	Gln	Ile	Phe	Arg	Asp	Phe	Ala	Glu	Asn	Lys	Gly	Lys	Phe	Ser
		35					40					45			
Val	Gly	Ala	Thr	Asn	Val	Leu	Val	Lys	Asp	Lys	Asn	Asn	Lys	Asp	Leu
		50				55						60			
Gly	Thr	Ala	Leu	Pro	Asn	Gly	Ile	Pro	Met	Ile	Asp	Phe	Ser	Val	Val
65					70					75					80
Asp	Val	Asp	Lys	Arg	Ile	Ala	Thr	Leu	Ile	Asn	Pro	Gln	Tyr	Val	Val
			85						90					95	
Gly	Val	Lys	His	Val	Ser	Asn	Gly	Val	Ser	Glu	Leu	His	Phe	Gly	Asn
			100					105					110		
Leu	Asn	Gly	Asn	Met	Asn	Asn	Gly	Asn	Ala	Lys	Ala	His	Arg	Asp	Val
		115					120					125			
Ser	Ser	Glu	Glu	Asn	Arg	Tyr	Phe	Ser	Val	Glu	Lys	Asn	Glu	Tyr	Pro
		130				135						140			

Thr	Lys	Leu	Asn	Gly	Lys	Thr	Val	Thr	Thr	Glu	Asp	Gln	Thr	Gln	Lys	145	150	155	160
Arg	Arg	Glu	Asp	Tyr	Tyr	Met	Pro	Arg	Leu	Asp	Lys	Phe	Val	Thr	Glu	165	170		175
Val	Ala	Pro	Ile	Glu	Ala	Ser	Thr	Ala	Ser	Ser	Asp	Ala	Gly	Thr	Tyr	180	185		190
Asn	Asp	Gln	Asn	Lys	Tyr	Pro	Ala	Phe	Val	Arg	Leu	Gly	Ser	Gly	Ser	195	200		205
Gln	Phe	Ile	Tyr	Lys	Lys	Gly	Asp	Asn	Tyr	Ser	Leu	Ile	Leu	Asn	Asn	210	215		220
His	Glu	Val	Gly	Gly	Asn	Asn	Leu	Lys	Leu	Val	Gly	Asp	Ala	Tyr	Thr	225	230		235
Tyr	Gly	Ile	Ala	Gly	Thr	Pro	Tyr	Lys	Val	Asn	His	Glu	Asn	Asn	Gly	245	250		255
Leu	Ile	Gly	Phe	Gly	Asn	Ser	Lys	Glu	Glu	His	Ser	Asp	Pro	Lys	Gly	260	265		270
Ile	Leu	Ser	Gln	Asp	Pro	Leu	Thr	Asn	Tyr	Ala	Val	Leu	Gly	Asp	Ser	275	280		285
Gly	Ser	Pro	Leu	Phe	Val	Tyr	Asp	Arg	Glu	Lys	Gly	Lys	Trp	Leu	Phe	290	295		300
Leu	Gly	Ser	Tyr	Asp	Phe	Trp	Ala	Gly	Tyr	Asn	Lys	Lys	Ser	Trp	Gln	305	310		315
Glu	Trp	Asn	Ile	Tyr	Lys	Ser	Gln	Phe	Thr	Lys	Asp	Val	Leu	Asn	Lys	325	330		335
Asp	Ser	Ala	Gly	Ser	Leu	Ile	Gly	Ser	Lys	Thr	Asp	Tyr	Ser	Trp	Ser	340	345		350
Ser	Asn	Gly	Lys	Thr	Ser	Thr	Ile	Thr	Gly	Gly	Glu	Lys	Ser	Leu	Asn	355	360		365
Val	Asp	Leu	Ala	Asp	Gly	Lys	Asp	Lys	Pro	Asn	His	Gly	Lys	Ser	Val	370	375		380
Thr	Phe	Glu	Gly	Ser	Gly	Thr	Leu	Thr	Leu	Asn	Asn	Asn	Ile	Asp	Gln	385	390		395
Gly	Ala	Gly	Gly	Leu	Phe	Phe	Glu	Gly	Asp	Tyr	Glu	Val	Lys	Gly	Thr	405	410		415
Ser	Asp	Asn	Thr	Thr	Trp	Lys	Gly	Ala	Gly	Val	Ser	Val	Ala	Glu	Gly	420	425		430
Lys	Thr	Val	Thr	Trp	Lys	Val	His	Asn	Pro	Gln	Tyr	Asp	Arg	Leu	Ala	435	440		445
Lys	Ile	Gly	Lys	Gly	Thr	Leu	Ile	Val	Glu	Gly	Thr	Gly	Asp	Asn	Lys	450	455		460
Gly	Ser	Leu	Lys	Val	Gly	Asp	Gly	Thr	Val	Ile	Leu	Lys	Gln	Gln	Thr	465	470		475
Asn	Gly	Ser	Gly	Gln	His	Ala	Phe	Ala	Ser	Val	Gly	Ile	Val	Ser	Gly	485	490		495
Arg	Ser	Thr	Leu	Val	Leu	Asn	Asp	Asp	Lys	Gln	Val	Asp	Pro	Asn	Ser				

500					505					510					
Ile	Tyr	Phe	Gly	Phe	Arg	Gly	Gly	Arg	Leu	Asp	Leu	Asn	Gly	Asn	Ser
		515					520					525			
Leu	Thr	Phe	Asp	His	Ile	Arg	Asn	Ile	Asp	Asp	Gly	Ala	Arg	Leu	Val
	530					535					540				
Asn	His	Asn	Met	Thr	Asn	Ala	Ser	Asn	Ile	Thr	Ile	Thr	Gly	Glu	Ser
545					550					555					560
Leu	Ile	Thr	Asp	Pro	Asn	Thr	Ile	Thr	Pro	Tyr	Asn	Ile	Asp	Ala	Pro
				565					570					575	
Asp	Glu	Asp	Asn	Pro	Tyr	Ala	Phe	Arg	Arg	Ile	Lys	Asp	Gly	Gly	Gln
			580					585					590		
Leu	Tyr	Leu	Asn	Leu	Glu	Asn	Tyr	Thr	Tyr	Tyr	Ala	Leu	Arg	Lys	Gly
	595						600					605			
Ala	Ser	Thr	Arg	Ser	Glu	Leu	Pro	Lys	Asn	Ser	Gly	Glu	Ser	Asn	Glu
	610					615					620				
Asn	Trp	Leu	Tyr	Met	Gly	Lys	Thr	Ser	Asp	Glu	Ala	Lys	Arg	Asn	Val
625					630					635					640
Met	Asn	His	Ile	Asn	Asn	Glu	Arg	Met	Asn	Gly	Phe	Asn	Gly	Tyr	Phe
				645					650					655	
Gly	Glu	Glu	Glu	Gly	Lys	Asn	Asn	Gly	Asn	Leu	Asn	Val	Thr	Phe	Lys
			660					665					670		
Gly	Lys	Ser	Glu	Gln	Asn	Arg	Phe	Leu	Leu	Thr	Gly	Gly	Thr	Asn	Leu
		675					680					685			
Asn	Gly	Asp	Leu	Thr	Val	Glu	Lys	Gly	Thr	Leu	Phe	Leu	Ser	Gly	Arg
	690					695					700				
Pro	Thr	Pro	His	Ala	Arg	Asp	Ile	Ala	Gly	Ile	Ser	Ser	Thr	Lys	Lys
705					710					715					720
Asp	Pro	His	Phe	Ala	Glu	Asn	Asn	Glu	Val	Val	Val	Glu	Asp	Asp	Trp
				725					730					735	
Ile	Asn	Arg	Asn	Phe	Lys	Ala	Thr	Thr	Met	Asn	Val	Thr	Gly	Asn	Ala
			740					745					750		
Ser	Leu	Tyr	Ser	Gly	Arg	Asn	Val	Ala	Asn	Ile	Thr	Ser	Asn	Ile	Thr
	755						760					765			
Ala	Ser	Asn	Lys	Ala	Gln	Val	His	Ile	Gly	Tyr	Lys	Thr	Gly	Asp	Thr
	770					775					780				
Val	Cys	Val	Arg	Ser	Asp	Tyr	Thr	Gly	Tyr	Val	Thr	Cys	Thr	Thr	Asp
785					790					795					800
Lys	Leu	Ser	Asp	Lys	Ala	Leu	Asn	Ser	Phe	Asn	Pro	Thr	Asn	Leu	Arg
				805					810					815	
Gly	Asn	Val	Asn	Leu	Thr	Glu	Ser	Ala	Asn	Phe	Val	Leu	Gly	Lys	Ala
			820					825					830		
Asn	Leu	Phe	Gly	Thr	Ile	Gln	Ser	Arg	Gly	Asn	Ser	Gln	Val	Arg	Leu
		835					840					845			
Thr	Glu	Asn	Ser	His	Trp	His	Leu	Thr	Gly	Asn	Ser	Asp	Val	His	Gln
	850					855						860			

Leu Asp Leu Ala Asn Gly His Ile His Leu Asn Ser Ala Asp Asn Ser
 865 870 875 880
 Asn Asn Val Thr Lys Tyr Asn Thr Leu Thr Val Asn Ser Leu Ser Gly
 885 890 895
 Asn Gly Ser Phe Tyr Tyr Leu Thr Asp Leu Ser Asn Lys Gln Gly Asp
 900 905 910
 Lys Val Val Val Thr Lys Ser Ala Thr Gly Asn Phe Thr Leu Gln Val
 915 920 925
 Ala Asp Lys Thr Gly Glu Pro Asn His Asn Glu Leu Thr Leu Phe Asp
 930 935 940
 Ala Ser Lys Ala Gln Arg Asp His Leu Asn Val Ser Leu Val Gly Asn
 945 950 955 960
 Thr Val Asp Leu Gly Ala Trp Lys Tyr Lys Leu Arg Asn Val Asn Gly
 965 970 975
 Arg Tyr Asp Leu Tyr Asn Pro Glu Val Glu Lys Arg Asn Gln Thr Val
 980 985 990
 Asp Thr Thr Asn Ile Thr Thr Pro Asn Asn Ile Gln Ala Asp Val Pro
 995 1000 1005
 Ser Val Pro Ser Asn Asn Glu Glu Ile Ala Arg Val Asp Glu Ala Pro
 1010 1015 1020
 Val Pro Pro Pro Ala Pro Ala Thr Pro Ser Glu Thr Thr Glu Thr Val
 1025 1030 1035 1040
 Ala Glu Asn Ser Lys Gln Glu Ser Lys Thr Val Glu Lys Asn Glu Gln
 1045 1050 1055
 Asp Ala Thr Glu Thr Thr Ala Gln Asn Arg Glu Val Ala Lys Glu Ala
 1060 1065 1070
 Lys Ser Asn Val Lys Ala Asn Thr Gln Thr Asn Glu Val Ala Gln Ser
 1075 1080 1085
 Gly Ser Glu Thr Lys Glu Thr Gln Thr Thr Glu Thr Lys Glu Thr Ala
 1090 1095 1100
 Thr Val Glu Lys Glu Glu Lys Ala Lys Val Glu Thr Glu Lys Thr Gln
 1105 1110 1115 1120
 Glu Val Pro Lys Val Thr Ser Gln Val Ser Pro Lys Gln Glu Gln Ser
 1125 1130 1135
 Glu Thr Val Gln Pro Gln Ala Glu Pro Ala Arg Glu Asn Asp Pro Thr
 1140 1145 1150
 Val Asn Ile Lys Glu Pro Gln Ser Gln Thr Asn Thr Thr Ala Asp Thr
 1155 1160 1165
 Glu Gln Pro Ala Lys Glu Thr Ser Ser Asn Val Glu Gln Pro Val Thr
 1170 1175 1180
 Glu Ser Thr Thr Val Asn Thr Gly Asn Ser Val Val Glu Asn Pro Glu
 1185 1190 1195 1200
 Asn Thr Thr Pro Ala Thr Thr Gln Pro Thr Val Asn Ser Glu Ser Ser
 1205 1210 1215
 Asn Lys Pro Lys Asn Arg His Arg Arg Ser Val Arg Ser Val Pro His

1220	1225	1230
Asn Val Glu Pro Ala Thr Thr Ser Ser Asn Asp Arg Ser Thr Val Ala 1235 1240 1245		
Leu Cys Asp Leu Thr Ser Thr Asn Thr Asn Ala Val Leu Ser Asp Ala 1250 1255 1260		
Arg Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly Lys Ala Val Ser 1265 1270 1275 1280		
Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly Gln Tyr Asn Val 1285 1290 1295		
Trp Val Ser Asn Thr Ser Met Asn Lys Asn Tyr Ser Ser Ser Gln Tyr 1300 1305 1310		
Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu Gly Trp Asp Gln 1315 1320 1325		
Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe Thr Tyr Val Arg 1330 1335 1340		
Asn Ser Asn Asn Phe Asp Lys Ala Thr Ser Lys Asn Thr Leu Ala Gln 1345 1350 1355 1360		
Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His Trp Tyr Leu Gly 1365 1370 1375		
Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Lys Leu Gln Thr Asn His 1380 1385 1390		
Asn Ala Lys Phe Ala Arg His Thr Ala Gln Phe Gly Leu Thr Ala Gly 1395 1400 1405		
Lys Ala Phe Asn Leu Gly Asn Phe Gly Ile Thr Pro Ile Val Gly Val 1410 1415 1420		
Arg Tyr Ser Tyr Leu Ser Asn Ala Asp Phe Ala Leu Asp Gln Ala Arg 1425 1430 1435 1440		
Ile Lys Val Asn Pro Ile Ser Val Lys Thr Ala Phe Ala Gln Val Asp 1445 1450 1455		
Leu Ser Tyr Thr Tyr His Leu Gly Glu Phe Ser Val Thr Pro Ile Leu 1460 1465 1470		
Ser Ala Arg Tyr Asp Ala Asn Gln Gly Ser Gly Lys Ile Asn Val Asn 1475 1480 1485		
Gly Tyr Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln Gln Tyr Asn Ala 1490 1495 1500		
Gly Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser Leu Ile Gly Gly 1505 1510 1515 1520		
Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr Ala Glu Leu Lys 1525 1530 1535		
Leu Ser Phe Ser Phe 1540		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Asn	Lys	Lys	Phe	Lys	Leu	Asn	Phe	Ile	Ala	Leu	Thr	Val	Ala
1				5					10					15	
Tyr	Ala	Leu	Thr	Pro	Tyr	Thr	Glu	Ala	Ala	Leu	Val	Arg	Asp	Asp	Val
			20					25					30		
Asp	Tyr	Gln	Ile	Phe	Arg	Asp	Phe	Ala	Glu	Asn	Lys	Gly	Lys	Phe	Ser
		35					40					45			
Val	Gly	Ala	Thr	Asn	Val	Glu	Val	Arg	Asp	Lys	Asn	Asn	Arg	Pro	Leu
	50					55					60				
Gly	Asn	Val	Leu	Pro	Asn	Gly	Ile	Pro	Met	Ile	Asp	Phe	Ser	Val	Val
65					70					75					80
Asp	Val	Asp	Lys	Arg	Ile	Ala	Thr	Leu	Val	Asn	Pro	Gln	Tyr	Val	Val
				85					90					95	
Gly	Val	Lys	His	Val	Ser	Asn	Gly	Val	Ser	Glu	Leu	His	Phe	Gly	Asn
			100					105					110		
Leu	Asn	Gly	Asn	Met	Asn	Asn	Gly	Asn	Ala	Lys	Ala	His	Arg	Asp	Val
		115					120					125			
Ser	Ser	Glu	Glu	Asn	Arg	Tyr	Tyr	Thr	Val	Glu	Lys	Asn	Glu	Tyr	Pro
	130					135					140				
Thr	Lys	Leu	Asn	Gly	Lys	Ala	Val	Thr	Thr	Glu	Asp	Gln	Ala	Gln	Lys
145					150					155					160
Arg	Arg	Glu	Asp	Tyr	Tyr	Met	Pro	Arg	Leu	Asp	Lys	Phe	Val	Thr	Glu
				165					170					175	
Val	Ala	Pro	Ile	Glu	Ala	Ser	Thr	Asp	Ser	Ser	Thr	Ala	Gly	Thr	Tyr
			180					185					190		
Asn	Asn	Lys	Asp	Lys	Tyr	Pro	Tyr	Phe	Val	Arg	Leu	Gly	Ser	Gly	Thr
		195					200					205			
Gln	Phe	Ile	Tyr	Glu	Asn	Gly	Thr	Arg	Tyr	Glu	Leu	Trp	Leu	Gly	Lys
	210					215					220				
Glu	Gly	Gln	Lys	Ser	Asp	Ala	Gly	Gly	Tyr	Asn	Leu	Lys	Leu	Val	Gly
225					230					235					240
Asn	Ala	Tyr	Thr	Tyr	Gly	Ile	Ala	Gly	Thr	Pro	Tyr	Glu	Val	Asn	His
				245					250					255	
Glu	Asn	Asp	Gly	Leu	Ile	Gly	Phe	Gly	Asn	Ser	Asn	Asn	Glu	Tyr	Ile
			260					265					270		
Asn	Pro	Lys	Glu	Ile	Leu	Ser	Lys	Lys	Pro	Leu	Thr	Asn	Tyr	Ala	Val
		275					280					285			
Leu	Gly	Asp	Ser	Gly	Ser	Pro	Leu	Phe	Val	Tyr	Asp	Arg	Glu	Lys	Gly
	290					295					300				
Lys	Trp	Leu	Phe	Leu	Gly	Ser	Tyr	Asp	Tyr	Trp	Ala	Gly	Tyr	Asn	Lys
305					310					315					320

Lys Ser Trp Gln Glu Trp Asn Ile Tyr Lys Pro Glu Phe Ala Glu Lys
 325 330 335
 Ile Tyr Glu Gln Tyr Ser Ala Gly Ser Leu Ile Gly Ser Lys Thr Asp
 340 345 350
 Tyr Ser Trp Ser Ser Asn Gly Lys Thr Ser Thr Ile Thr Gly Gly Glu
 355 360 365
 Lys Ser Leu Asn Val Asp Leu Ala Asp Gly Lys Asp Lys Pro Asn His
 370 375 380
 Gly Lys Ser Val Thr Phe Glu Gly Ser Gly Thr Leu Thr Leu Asn Asn
 385 390 395 400
 Asn Ile Asp Gln Gly Ala Gly Gly Leu Phe Phe Glu Gly Asp Tyr Glu
 405 410 415
 Val Lys Gly Thr Ser Asp Asn Thr Thr Trp Lys Gly Ala Gly Val Ser
 420 425 430
 Val Ala Glu Gly Lys Thr Val Thr Trp Lys Val His Asn Pro Gln Tyr
 435 440 445
 Asp Arg Leu Ala Lys Ile Gly Lys Gly Thr Leu Ile Val Glu Gly Thr
 450 455 460
 Gly Asp Asn Lys Gly Ser Leu Lys Val Gly Asp Gly Thr Val Ile Leu
 465 470 475 480
 Lys Gln Gln Thr Asn Gly Ser Gly Gln His Ala Phe Ala Ser Val Gly
 485 490 495
 Ile Val Ser Gly Arg Ser Thr Leu Val Leu Asn Asp Asp Lys Gln Val
 500 505 510
 Asp Pro Asn Ser Ile Tyr Phe Gly Phe Arg Gly Gly Arg Leu Asp Leu
 515 520 525
 Asn Gly Asn Ser Leu Thr Phe Asp His Ile Arg Asn Ile Asp Glu Gly
 530 535 540
 Ala Arg Leu Val Asn His Ser Thr Ser Lys His Ser Thr Val Thr Ile
 545 550 555 560
 Thr Gly Asp Asn Leu Ile Thr Asp Pro Asn Asn Val Ser Ile Tyr Tyr
 565 570 575
 Val Lys Pro Leu Glu Asp Asp Asn Pro Tyr Ala Ile Arg Gln Ile Lys
 580 585 590
 Tyr Gly Tyr Gln Leu Tyr Phe Asn Glu Glu Asn Arg Thr Tyr Tyr Ala
 595 600 605
 Leu Lys Lys Asp Ala Ser Ile Arg Ser Glu Phe Pro Gln Asn Arg Gly
 610 615 620
 Glu Ser Asn Asn Ser Trp Leu Tyr Met Gly Thr Glu Lys Ala Asp Ala
 625 630 635 640
 Gln Lys Asn Ala Met Asn His Ile Asn Asn Glu Arg Met Asn Gly Phe
 645 650 655
 Asn Gly Tyr Phe Gly Glu Glu Glu Gly Lys Asn Asn Gly Asn Leu Asn
 660 665 670
 Val Thr Phe Lys Gly Lys Ser Glu Gln Asn Arg Phe Leu Leu Thr Gly

675					680					685					
Gly	Thr	Asn	Leu	Asn	Gly	Asp	Leu	Asn	Val	Gln	Gln	Gly	Thr	Leu	Phe
690					695					700					
Leu	Ser	Gly	Arg	Pro	Thr	Pro	His	Ala	Arg	Asp	Ile	Ala	Gly	Ile	Ser
705					710					715					720
Ser	Thr	Lys	Lys	Asp	Ser	His	Phe	Ser	Glu	Asn	Asn	Glu	Val	Val	Val
				725					730					735	
Glu	Asp	Asp	Trp	Ile	Asn	Arg	Asn	Phe	Lys	Ala	Thr	Asn	Ile	Asn	Val
			740					745					750		
Thr	Asn	Asn	Ala	Thr	Leu	Tyr	Ser	Gly	Arg	Asn	Val	Glu	Ser	Ile	Thr
			755				760					765			
Ser	Asn	Ile	Thr	Ala	Ser	Asn	Asn	Ala	Lys	Val	His	Ile	Gly	Tyr	Lys
			770				775					780			
Ala	Gly	Asp	Thr	Val	Cys	Val	Arg	Ser	Asp	Tyr	Thr	Gly	Tyr	Val	Thr
785					790					795					800
Cys	Thr	Thr	Asp	Lys	Leu	Ser	Asp	Lys	Ala	Leu	Asn	Ser	Phe	Asn	Pro
				805					810					815	
Thr	Asn	Leu	Arg	Gly	Asn	Val	Asn	Leu	Thr	Glu	Ser	Ala	Asn	Phe	Val
			820					825					830		
Leu	Gly	Lys	Ala	Asn	Leu	Phe	Gly	Thr	Ile	Gln	Ser	Arg	Gly	Asn	Ser
		835					840					845			
Gln	Val	Arg	Leu	Thr	Glu	Asn	Ser	His	Trp	His	Leu	Thr	Gly	Asn	Ser
							855					860			
Asp	Val	His	Gln	Leu	Asp	Leu	Ala	Asn	Gly	His	Ile	His	Leu	Asn	Ser
865							870					875			880
Ala	Asp	Asn	Ser	Asn	Asn	Val	Thr	Lys	Tyr	Asn	Thr	Leu	Thr	Val	Asn
				885					890					895	
Ser	Leu	Ser	Gly	Asn	Gly	Ser	Phe	Tyr	Tyr	Leu	Thr	Asp	Leu	Ser	Asn
			900					905					910		
Lys	Gln	Gly	Asp	Lys	Val	Val	Val	Thr	Lys	Ser	Ala	Thr	Gly	Asn	Phe
			915				920					925			
Thr	Leu	Gln	Val	Ala	Asp	Lys	Thr	Gly	Glu	Pro	Asn	His	Asn	Glu	Leu
							935					940			
Thr	Leu	Phe	Asp	Ala	Ser	Lys	Ala	Gln	Arg	Asp	His	Leu	Asn	Val	Ser
945							950					955			960
Leu	Val	Gly	Asn	Thr	Val	Asp	Leu	Gly	Ala	Trp	Lys	Tyr	Lys	Leu	Arg
				965					970					975	
Asn	Val	Asn	Gly	Arg	Tyr	Asp	Leu	Tyr	Asn	Pro	Glu	Val	Glu	Lys	Arg
			980					985					990		
Asn	Gln	Thr	Val	Asp	Thr	Thr	Asn	Ile	Thr	Thr	Pro	Asn	Asn	Ile	Gln
			995				1000					1005			
Ala	Asp	Val	Pro	Ser	Val	Pro	Ser	Asn	Asn	Glu	Glu	Ile	Ala	Arg	Val
			1010				1015					1020			
Asp	Glu	Ala	Pro	Val	Pro	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Ser	Glu	Thr
1025							1030					1035			1040

Thr Glu Thr Val Ala Glu Asn Ser Lys Gln Glu Ser Lys Thr Val Glu
 1045 1050 1055
 Lys Asn Glu Gln Asp Ala Thr Glu Thr Thr Ala Gln Asn Arg Glu Val
 1060 1065 1070
 Ala Lys Glu Ala Lys Ser Asn Val Lys Ala Asn Thr Gln Thr Asn Glu
 1075 1080 1085
 Val Ala Gln Ser Gly Ser Glu Thr Lys Glu Thr Gln Thr Thr Glu Thr
 1090 1095 1100
 Lys Glu Thr Ala Thr Val Glu Lys Glu Glu Lys Ala Lys Val Glu Thr
 1105 1110 1115 1120
 Glu Lys Thr Gln Glu Val Pro Lys Val Thr Ser Gln Val Ser Pro Lys
 1125 1130 1135
 Gln Glu Gln Ser Glu Thr Val Gln Pro Gln Ala Glu Pro Ala Arg Glu
 1140 1145 1150
 Asn Asp Pro Thr Val Asn Ile Lys Glu Pro Gln Ser Gln Thr Asn Thr
 1155 1160 1165
 Thr Ala Asp Thr Glu Gln Pro Ala Lys Glu Thr Ser Ser Asn Val Glu
 1170 1175 1180
 Gln Pro Val Thr Glu Ser Thr Thr Val Asn Thr Gly Asn Ser Val Val
 1185 1190 1195 1200
 Glu Asn Pro Glu Asn Thr Thr Pro Ala Thr Thr Gln Pro Thr Val Asn
 1205 1210 1215
 Ser Glu Ser Ser Asn Lys Pro Lys Asn Arg His Arg Arg Ser Val Arg
 1220 1225 1230
 Ser Val Pro His Asn Val Glu Pro Ala Thr Thr Ser Ser Asn Asp Arg
 1235 1240 1245
 Ser Thr Val Ala Leu Cys Asp Leu Thr Ser Thr Asn Thr Asn Ala Val
 1250 1255 1260
 Leu Ser Asp Ala Arg Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly
 1265 1270 1275 1280
 Lys Ala Val Ser Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly
 1285 1290 1295
 Gln Tyr Asn Val Trp Val Ser Asn Thr Ser Met Asn Lys Asn Tyr Ser
 1300 1305 1310
 Ser Ser Gln Tyr Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu
 1315 1320 1325
 Gly Trp Asp Gln Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe
 1330 1335 1340
 Thr Tyr Val Arg Asn Ser Asn Asn Phe Asp Lys Ala Thr Ser Lys Asn
 1345 1350 1355 1360
 Thr Leu Ala Gln Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His
 1365 1370 1375
 Trp Tyr Leu Gly Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Lys Leu
 1380 1385 1390
 Gln Thr Asn His Asn Ala Lys Phe Ala Arg His Thr Ala Gln Phe Gly

1395	1400	1405
Leu Thr Ala Gly Lys Ala 1410	Phe Asn Leu Gly Asn 1415	Phe Gly Ile Thr Pro 1420
Ile Val Gly Val Arg Tyr Ser Tyr 1425	Leu Ser Asn Ala Asp Phe Ala Leu 1430 1435 1440	
Asp Gln Ala Arg Ile Lys Val Asn Pro 1445	Ile Ser Val Lys Thr Ala Phe 1450 1455	
Ala Gln Val Asp Leu Ser Tyr Thr 1460	Tyr His Leu Gly Glu Phe Ser Val 1465 1470	
Thr Pro Ile Leu Ser Ala Arg Tyr Asp 1475 1480	Ala Asn Gln Gly Ser Gly Lys 1485	
Ile Asn Val Asn Gly Tyr Asp Phe Ala Tyr 1490 1495	Asn Val Glu Asn Gln Gln 1500	
Gln Tyr Asn Ala Gly Leu Lys Leu Lys Tyr 1505 1510	His Asn Val Lys Leu Ser 1515 1520	
Leu Ile Gly Gly Leu Thr Lys Ala Lys 1525	Gln Ala Glu Lys Gln Lys Thr 1530 1535	
Ala Glu Leu Lys Leu Ser Phe Ser 1540	Phe 1545	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1702 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Leu Asn Lys Lys Phe Lys Leu Asn Phe Ile Ala Leu Thr Val Ala 1 5 10 15
Tyr Ala Leu Thr Pro Tyr Thr Glu Ala Ala Leu Val Arg Asp Asp Val 20 25 30
Asp Tyr Gln Ile Phe Arg Asp Phe Ala Glu Asn Lys Gly Arg Phe Ser 35 40 45
Val Gly Ala Thr Asn Val Glu Val Arg Asp Lys Asn Asn His Ser Leu 50 55 60
Gly Asn Val Leu Pro Asn Gly Ile Pro Met Ile Asp Phe Ser Val Val 65 70 75 80
Asp Val Asp Lys Arg Ile Ala Thr Leu Ile Asn Pro Gln Tyr Val Val 85 90 95
Gly Val Lys His Val Ser Asn Gly Val Ser Glu Leu His Phe Gly Asn 100 105 110
Leu Asn Gly Asn Met Asn Asn Gly Asn Asp Lys Ser His Arg Asp Val 115 120 125
Ser Ser Glu Glu Asn Arg Tyr Phe Ser Val Glu Lys Asn Glu Tyr Pro 130 135 140
Thr Lys Leu Asn Gly Lys Ala Val Thr Thr Glu Asp Gln Thr Gln Lys

145					150					155					160				
Arg	Arg	Glu	Asp	Tyr 165	Tyr	Met	Pro	Arg	Leu 170	Asp	Lys	Phe	Val	Thr 175	Glu				
Val	Ala	Pro	Ile 180	Glu	Ala	Ser	Thr	Ala 185	Ser	Ser	Asp	Ala	Gly 190	Thr	Tyr				
Asn	Asp	Gln 195	Asn	Lys	Tyr	Pro	Ala 200	Phe	Val	Arg	Leu	Gly 205	Ser	Gly	Thr				
Gln	Phe 210	Ile	Tyr	Lys	Lys	Gly 215	Asp	Asn	Tyr	Ser	Leu 220	Ile	Leu	Asn	Asn				
His 225	Glu	Val	Gly	Gly	Asn 230	Asn	Leu	Lys	Leu	Val 235	Gly	Asp	Ala	Tyr	Thr 240				
Tyr	Gly	Ile	Ala	Gly 245	Thr	Pro	Tyr	Lys	Val 250	Asn	His	Glu	Asn	Asn	Gly 255				
Leu	Ile	Gly	Phe 260	Gly	Asn	Ser	Lys	Glu 265	Glu	His	Ser	Asp	Pro 270	Lys	Gly				
Ile	Leu	Ser	Gln 275	Asp	Pro	Leu	Thr 280	Asn	Tyr	Ala	Val	Leu 285	Gly	Asp	Ser				
Gly 290	Ser	Pro	Leu	Phe	Val	Tyr 295	Asp	Arg	Glu	Lys	Gly 300	Lys	Trp	Leu	Phe				
Leu 305	Gly	Ser	Tyr	Asp	Phe 310	Trp	Ala	Gly	Tyr	Asn 315	Lys	Lys	Ser	Trp	Gln 320				
Glu	Trp	Asn	Ile 325	Tyr	Lys	Pro	Glu	Phe 330	Lys	Thr	Val	Leu 335	Asp	Lys					
Asp	Thr	Ala	Gly 340	Ser	Leu	Ile	Gly	Ser 345	Asn	Thr	Gln	Tyr	Asn 350	Trp	Asn				
Pro	Thr	Gly 355	Lys	Thr	Ser	Val	Ile 360	Ser	Asn	Gly	Ser	Glu 365	Ser	Leu	Asn				
Val	Asp 370	Leu	Phe	Asp	Ser	Ser 375	Gln	Asp	Thr	Asp	Ser 380	Lys	Lys	Asn	Asn				
His 385	Gly	Lys	Ser	Val	Thr 390	Leu	Arg	Gly	Ser	Gly 395	Thr	Leu	Thr	Leu	Asn 400				
Asn	Asn	Ile	Asp	Gln 405	Gly	Ala	Gly	Gly	Leu 410	Phe	Phe	Glu	Gly	Asp 415	Tyr				
Glu	Val	Lys	Gly 420	Thr	Ser	Asp	Ser	Thr 425	Thr	Trp	Lys	Gly	Ala 430	Gly	Val				
Ser	Val	Ala 435	Asp	Gly	Lys	Thr	Val 440	Thr	Trp	Lys	Val	His 445	Asn	Pro	Lys				
Ser	Asp 450	Arg	Leu	Ala	Lys	Ile 455	Gly	Lys	Gly	Thr	Leu 460	Ile	Val	Glu	Gly				
Lys 465	Gly	Glu	Asn	Lys	Gly 470	Ser	Leu	Lys	Val	Gly 475	Asp	Gly	Thr	Val	Ile 480				
Leu	Lys	Gln	Gln	Ala 485	Asp	Ala	Asn	Asn	Lys 490	Val	Lys	Ala	Phe	Ser 495	Gln				
Val	Gly	Ile	Val 500	Ser	Gly	Arg	Ser	Thr 505	Val	Val	Leu	Asn	Asp 510	Asp	Lys				

Gln Val Asp Pro Asn Ser Ile Tyr Phe Gly Phe Arg Gly Gly Arg Leu
 515 520 525
 Asp Ala Asn Gly Asn Asn Leu Thr Phe Glu His Ile Arg Asn Ile Asp
 530 535 540
 Asp Gly Ala Arg Leu Val Asn His Asn Thr Ser Lys Thr Ser Thr Val
 545 550 555 560
 Thr Ile Thr Gly Glu Ser Leu Ile Thr Asp Pro Asn Thr Ile Thr Pro
 565 570 575
 Tyr Asn Ile Asp Ala Pro Asp Glu Asp Asn Pro Tyr Ala Phe Arg Arg
 580 585 590
 Ile Lys Asp Gly Gly Gln Leu Tyr Leu Asn Leu Glu Asn Tyr Thr Tyr
 595 600 605
 Tyr Ala Leu Arg Lys Gly Ala Ser Thr Arg Ser Glu Leu Pro Lys Asn
 610 615 620
 Ser Gly Glu Ser Asn Glu Asn Trp Leu Tyr Met Gly Lys Thr Ser Asp
 625 630 635 640
 Ala Ala Lys Arg Asn Val Met Asn His Ile Asn Asn Glu Arg Met Asn
 645 650 655
 Gly Phe Asn Gly Tyr Phe Gly Glu Glu Glu Gly Lys Asn Asn Gly Asn
 660 665 670
 Leu Asn Val Thr Phe Lys Gly Lys Ser Glu Gln Asn Arg Phe Leu Leu
 675 680 685
 Thr Gly Gly Thr Asn Leu Asn Gly Asp Leu Lys Val Glu Lys Gly Thr
 690 695 700
 Leu Phe Leu Ser Gly Arg Pro Thr Pro His Ala Arg Asp Ile Ala Gly
 705 710 715 720
 Ile Ser Ser Thr Lys Lys Asp Gln His Phe Ala Glu Asn Asn Glu Val
 725 730 735
 Val Val Glu Asp Asp Trp Ile Asn Arg Asn Phe Lys Ala Thr Asn Ile
 740 745 750
 Asn Val Thr Asn Asn Ala Thr Leu Tyr Ser Gly Arg Asn Val Ala Asn
 755 760 765
 Ile Thr Ser Asn Ile Thr Ala Ser Asp Asn Ala Lys Val His Ile Gly
 770 775 780
 Tyr Lys Ala Gly Asp Thr Val Cys Val Arg Ser Asp Tyr Thr Gly Tyr
 785 790 795 800
 Val Thr Cys Thr Thr Asp Lys Leu Ser Asp Lys Ala Leu Asn Ser Phe
 805 810 815
 Asn Ala Thr Asn Val Ser Gly Asn Val Asn Leu Ser Gly Asn Ala Asn
 820 825 830
 Phe Val Leu Gly Lys Ala Asn Leu Phe Gly Thr Ile Ser Gly Thr Gly
 835 840 845
 Asn Ser Gln Val Arg Leu Thr Glu Asn Ser His Trp His Leu Thr Gly
 850 855 860
 Asp Ser Asn Val Asn Gln Leu Asn Leu Asp Lys Gly His Ile His Leu

865						870						875						880
Asn	Ala	Gln	Asn	Asp	Ala	Asn	Lys	Val	Thr	Thr	Tyr	Asn	Thr	Leu	Thr			
				885					890					895				
Val	Asn	Ser	Leu	Ser	Gly	Asn	Gly	Ser	Phe	Tyr	Tyr	Leu	Thr	Asp	Leu			
			900					905					910					
Ser	Asn	Lys	Gln	Gly	Asp	Lys	Val	Val	Val	Thr	Lys	Ser	Ala	Thr	Gly			
		915					920					925						
Asn	Phe	Thr	Leu	Gln	Val	Ala	Asp	Lys	Thr	Gly	Glu	Pro	Thr	Lys	Asn			
	930					935					940							
Glu	Leu	Thr	Leu	Phe	Asp	Ala	Ser	Asn	Ala	Thr	Arg	Asn	Asn	Leu	Asn			
945					950					955					960			
Val	Ser	Leu	Val	Gly	Asn	Thr	Val	Asp	Leu	Gly	Ala	Trp	Lys	Tyr	Lys			
				965					970					975				
Leu	Arg	Asn	Val	Asn	Gly	Arg	Tyr	Asp	Leu	Tyr	Asn	Pro	Glu	Val	Glu			
			980					985					990					
Lys	Arg	Asn	Gln	Thr	Val	Asp	Thr	Thr	Asn	Ile	Thr	Thr	Pro	Asn	Asn			
		995					1000						1005					
Ile	Gln	Ala	Asp	Val	Pro	Ser	Val	Pro	Ser	Asn	Asn	Glu	Glu	Ile	Ala			
	1010						1015					1020						
Arg	Val	Glu	Thr	Pro	Val	Pro	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Ser	Glu			
1025					1030					1035					1040			
Thr	Thr	Glu	Thr	Val	Ala	Glu	Asn	Ser	Lys	Gln	Glu	Ser	Lys	Thr	Val			
				1045					1050					1055				
Glu	Lys	Asn	Glu	Gln	Asp	Ala	Thr	Glu	Thr	Thr	Ala	Gln	Asn	Gly	Glu			
			1060					1065					1070					
Val	Ala	Glu	Glu	Ala	Lys	Pro	Ser	Val	Lys	Ala	Asn	Thr	Gln	Thr	Asn			
		1075					1080					1085						
Glu	Val	Ala	Gln	Ser	Gly	Ser	Glu	Thr	Glu	Glu	Thr	Gln	Thr	Thr	Glu			
	1090					1095					1100							
Ile	Lys	Glu	Thr	Ala	Lys	Val	Glu	Lys	Glu	Glu	Lys	Ala	Lys	Val	Glu			
1105					1110					1115					1120			
Lys	Glu	Glu	Lys	Ala	Lys	Val	Glu	Lys	Asp	Glu	Ile	Gln	Glu	Ala	Pro			
				1125					1130					1135				
Gln	Met	Ala	Ser	Glu	Thr	Ser	Pro	Lys	Gln	Ala	Lys	Pro	Ala	Pro	Lys			
			1140					1145					1150					
Glu	Val	Ser	Thr	Asp	Thr	Lys	Val	Glu	Glu	Thr	Gln	Val	Gln	Ala	Gln			
		1155					1160					1165						
Pro	Gln	Thr	Gln	Ser	Thr	Thr	Val	Ala	Ala	Ala	Glu	Ala	Thr	Ser	Pro			
		1170				1175						1180						
Asn	Ser	Lys	Pro	Ala	Glu	Glu	Thr	Gln	Pro	Ser	Glu	Lys	Thr	Asn	Ala			
1185					1190					1195					1200			
Glu	Pro	Val	Thr	Pro	Val	Val	Ser	Lys	Asn	Gln	Thr	Glu	Asn	Thr	Thr			
				1205					1210					1215				
Asp	Gln	Pro	Thr	Glu	Arg	Glu	Lys	Thr	Ala	Lys	Val	Glu	Thr	Glu	Lys			
			1220					1225					1230					

Thr Gln Glu Pro Pro Gln Val Ala Ser Gln Ala Ser Pro Lys Gln Glu
 1235 1240 1245
 Gln Ser Glu Thr Val Gln Pro Gln Ala Val Leu Glu Ser Glu Asn Val
 1250 1255 1260
 Pro Thr Val Asn Asn Ala Glu Glu Val Gln Ala Gln Leu Gln Thr Gln
 1265 1270 1275 1280
 Thr Ser Ala Thr Val Ser Thr Lys Gln Pro Ala Pro Glu Asn Ser Ile
 1285 1290 1295
 Asn Thr Gly Ser Ala Thr Ala Ile Thr Glu Thr Ala Glu Lys Ser Asp
 1300 1305 1310
 Lys Pro Gln Thr Glu Thr Ala Ala Ser Thr Glu Asp Ala Ser Gln His
 1315 1320 1325
 Lys Ala Asn Thr Val Ala Asp Asn Ser Val Ala Asn Asn Ser Glu Ser
 1330 1335 1340
 Ser Glu Pro Lys Ser Arg Arg Arg Arg Ser Ile Ser Gln Pro Gln Glu
 1345 1350 1355 1360
 Thr Ser Ala Glu Glu Thr Thr Ala Ala Ser Thr Asp Glu Thr Thr Ile
 1365 1370 1375
 Ala Asp Asn Ser Lys Arg Ser Lys Pro Asn Arg Arg Ser Arg Arg Ser
 1380 1385 1390
 Val Arg Ser Glu Pro Thr Val Thr Asn Gly Ser Asp Arg Ser Thr Val
 1395 1400 1405
 Ala Leu Arg Asp Leu Thr Ser Thr Asn Thr Asn Ala Val Ile Ser Asp
 1410 1415 1420
 Ala Met Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly Lys Ala Val
 1425 1430 1435 1440
 Ser Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly Gln Tyr Asn
 1445 1450 1455
 Val Trp Val Ser Asn Thr Ser Met Asn Glu Asn Tyr Ser Ser Ser Gln
 1460 1465 1470
 Tyr Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu Gly Trp Asp
 1475 1480 1485
 Gln Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe Thr Tyr Val
 1490 1495 1500
 Arg Asn Ser Asn Asn Phe Asp Lys Ala Ser Ser Lys Asn Thr Leu Ala
 1505 1510 1515 1520
 Gln Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His Trp Tyr Leu
 1525 1530 1535
 Gly Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Asn Leu Lys Thr Asn
 1540 1545 1550
 His Asn Ala Lys Phe Ala Arg His Thr Ala Gln Phe Gly Leu Thr Ala
 1555 1560 1565
 Gly Lys Ala Phe Asn Leu Gly Asn Phe Gly Ile Thr Pro Ile Val Gly
 1570 1575 1580
 Val Arg Tyr Ser Tyr Leu Ser Asn Ala Asn Phe Ala Leu Ala Lys Asp

1585	1590	1595	1600
Arg Ile Lys Val Asn Pro Ile Ser Val Lys Thr Ala Phe Ala Gln Val	1605	1610	1615
Asp Leu Ser Tyr Thr Tyr His Leu Gly Glu Phe Ser Val Thr Pro Ile	1620	1625	1630
Leu Ser Ala Arg Tyr Asp Thr Asn Gln Gly Ser Gly Lys Ile Asn Val	1635	1640	1645
Asn Gln Tyr Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln Gln Tyr Asn	1650	1655	1660
Ala Gly Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser Leu Ile Gly	1665	1670	1675
Gly Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr Ala Glu Leu	1685	1690	1695
Lys Leu Ser Phe Ser Phe	1700		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1848 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Asn Lys Lys Phe Lys Leu Asn Phe Ile Ala Leu Thr Val Ala	1	5	10	15
Tyr Ala Leu Thr Pro Tyr Thr Glu Ala Ala Leu Val Arg Asp Asp Val	20	25	30	
Asp Tyr Gln Ile Phe Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe Ser	35	40	45	
Val Gly Ala Thr Asn Val Glu Val Arg Asp Lys Lys Asn Gln Ser Leu	50	55	60	
Gly Ser Ala Leu Pro Asn Gly Ile Pro Met Ile Asp Phe Ser Val Val	65	70	75	80
Asp Val Asp Lys Arg Ile Ala Thr Leu Val Asn Pro Gln Tyr Val Val	85	90	95	
Gly Val Lys His Val Ser Asn Gly Val Ser Glu Leu His Phe Gly Asn	100	105	110	
Leu Asn Gly Asn Met Asn Asn Gly Asn Ala Lys Ser His Arg Asp Val	115	120	125	
Ser Ser Glu Glu Asn Arg Tyr Tyr Thr Val Glu Lys Asn Asn Phe Pro	130	135	140	
Thr Glu Asn Val Thr Ser Phe Thr Lys Glu Glu Gln Asp Ala Gln Lys	145	150	155	160
Arg Arg Glu Asp Tyr Tyr Met Pro Arg Leu Asp Lys Phe Val Thr Glu	165	170		175
Val Ala Pro Ile Glu Ala Ser Thr Ala Asn Asn Asn Lys Gly Glu Tyr				

180							185							190																	
Asn	Asn	Ser	Asp	Lys	Tyr	Pro	Ala	Phe	Val	Arg	Leu	Gly	Ser	Gly	Thr	Asn	Asn	Ser	Asp	Lys	Tyr	Pro	Ala	Phe	Val	Arg	Leu	Gly	Ser	Gly	Thr
		195					200					205																210			
Gln	Phe	Ile	Tyr	Lys	Lys	Gly	Ser	Arg	Tyr	Gln	Leu	Ile	Leu	Thr	Glu													215			
Lys	Asp	Lys	Gln	Gly	Asn	Leu	Leu	Arg	Asn	Trp	Asp	Val	Gly	Gly	Asp													220			
Asn	Leu	Glu	Leu	Val	Gly	Asn	Ala	Tyr	Thr	Tyr	Gly	Ile	Ala	Gly	Thr													225			
Pro	Tyr	Lys	Val	Asn	His	Glu	Asn	Asn	Gly	Leu	Ile	Gly	Phe	Gly	Asn													230			
Ser	Lys	Glu	Glu	His	Ser	Asp	Pro	Lys	Gly	Ile	Leu	Ser	Gln	Asp	Pro													235			
Leu	Thr	Asn	Tyr	Ala	Val	Leu	Gly	Asp	Ser	Gly	Ser	Pro	Leu	Phe	Val													240			
Tyr	Asp	Arg	Glu	Lys	Gly	Lys	Trp	Leu	Phe	Leu	Gly	Ser	Tyr	Asp	Phe													245			
Trp	Ala	Gly	Tyr	Asn	Lys	Lys	Ser	Trp	Gln	Glu	Trp	Asn	Ile	Tyr	Lys													250			
His	Glu	Phe	Ala	Glu	Lys	Ile	Tyr	Gln	Gln	Tyr	Ser	Ala	Gly	Ser	Leu													255			
Ile	Gly	Ser	Asn	Thr	Gln	Tyr	Thr	Trp	Gln	Ala	Thr	Gly	Ser	Thr	Ser													260			
Thr	Ile	Thr	Gly	Gly	Gly	Glu	Pro	Leu	Ser	Val	Asp	Leu	Thr	Asp	Gly													265			
Lys	Asp	Lys	Pro	Asn	His	Gly	Lys	Ser	Ile	Thr	Leu	Lys	Gly	Ser	Gly													270			
Thr	Leu	Thr	Leu	Asn	Asn	His	Ile	Asp	Gln	Gly	Ala	Gly	Gly	Leu	Phe													275			
Phe	Glu	Gly	Asp	Tyr	Glu	Val	Lys	Gly	Thr	Ser	Asp	Ser	Thr	Thr	Trp													280			
Lys	Gly	Ala	Gly	Val	Ser	Val	Ala	Asp	Gly	Lys	Thr	Val	Thr	Trp	Lys													285			
Val	His	Asn	Pro	Lys	Tyr	Asp	Arg	Leu	Ala	Lys	Ile	Gly	Lys	Gly	Thr													290			
Leu	Val	Val	Glu	Gly	Lys	Gly	Lys	Asn	Glu	Gly	Leu	Leu	Lys	Val	Gly													295			
Asp	Gly	Thr	Val	Ile	Leu	Lys	Gln	Lys	Ala	Asp	Ala	Asn	Asn	Lys	Val													300			
Gln	Ala	Phe	Ser	Gln	Val	Gly	Ile	Val	Ser	Gly	Arg	Ser	Thr	Leu	Val													305			
Leu	Asn	Asp	Asp	Lys	Gln	Val	Asp	Pro	Asn	Ser	Ile	Tyr	Phe	Gly	Phe													310			
Arg	Gly	Gly	Arg	Leu																											

Ile Arg Asn Ile Asp Asp Gly Ala Arg Val Val Asn His Asn Met Thr
 545 550 555 560
 Asn Thr Ser Asn Ile Thr Ile Thr Gly Glu Ser Leu Ile Thr Asn Pro
 565 570 575
 Asn Thr Ile Thr Ser Tyr Asn Ile Glu Ala Gln Asp Asp Asp His Pro
 580 585 590
 Leu Arg Ile Arg Ser Ile Pro Tyr Arg Gln Leu Tyr Phe Asn Gln Asp
 595 600 605
 Asn Arg Ser Tyr Tyr Thr Leu Lys Lys Gly Ala Ser Thr Arg Ser Glu
 610 615 620
 Leu Pro Gln Asn Ser Gly Glu Ser Asn Glu Asn Trp Leu Tyr Met Gly
 625 630 635 640
 Arg Thr Ser Asp Ala Ala Lys Arg Asn Val Met Asn His Ile Asn Asn
 645 650 655
 Glu Arg Met Asn Gly Phe Asn Gly Tyr Phe Gly Glu Glu Glu Thr Lys
 660 665 670
 Ala Thr Gln Asn Gly Lys Leu Asn Val Thr Phe Asn Gly Lys Ser Asp
 675 680 685
 Gln Asn Arg Phe Leu Leu Thr Gly Gly Thr Asn Leu Asn Gly Asp Leu
 690 695 700
 Asn Val Glu Lys Gly Thr Leu Phe Leu Ser Gly Arg Pro Thr Pro His
 705 710 715 720
 Ala Arg Asp Ile Ala Gly Ile Ser Ser Thr Lys Lys Asp Pro His Phe
 725 730 735
 Thr Glu Asn Asn Glu Val Val Val Glu Asp Asp Trp Ile Asn Arg Asn
 740 745 750
 Phe Lys Ala Thr Thr Met Asn Val Thr Gly Asn Ala Ser Leu Tyr Ser
 755 760 765
 Gly Arg Asn Val Ala Asn Ile Thr Ser Asn Ile Thr Ala Ser Asn Asn
 770 775 780
 Ala Gln Val His Ile Gly Tyr Lys Thr Gly Asp Thr Val Cys Val Arg
 785 790 795 800
 Ser Asp Tyr Thr Gly Tyr Val Thr Cys His Asn Ser Asn Leu Ser Glu
 805 810 815
 Lys Ala Leu Asn Ser Phe Asn Pro Thr Asn Leu Arg Gly Asn Val Asn
 820 825 830
 Leu Thr Glu Asn Ala Ser Phe Thr Leu Gly Lys Ala Asn Leu Phe Gly
 835 840 845
 Thr Ile Gln Ser Ile Gly Thr Ser Gln Val Asn Leu Lys Glu Asn Ser
 850 855 860
 His Trp His Leu Thr Gly Asn Ser Asn Val Asn Gln Leu Asn Leu Thr
 865 870 875 880
 Asn Gly His Ile His Leu Asn Ala Gln Asn Asp Ala Asn Lys Val Thr
 885 890 895
 Thr Tyr Asn Thr Leu Thr Val Asn Ser Leu Ser Gly Asn Gly Ser Phe

900										905					910				
Tyr	Tyr	Trp	Val	Asp	Phe	Thr	Asn	Asn	Lys	Ser	Asn	Lys	Val	Val	Val				
		915					920					925							
Asn	Lys	Ser	Ala	Thr	Gly	Asn	Phe	Thr	Leu	Gln	Val	Ala	Asp	Lys	Thr				
	930					935					940								
Gly	Glu	Pro	Asn	His	Asn	Glu	Leu	Thr	Leu	Phe	Asp	Ala	Ser	Asn	Ala				
945					950					955					960				
Thr	Arg	Asn	Asn	Leu	Glu	Val	Thr	Leu	Ala	Asn	Gly	Ser	Val	Asp	Arg				
				965				970						975					
Gly	Ala	Trp	Lys	Tyr	Lys	Leu	Arg	Asn	Val	Asn	Gly	Arg	Tyr	Asp	Leu				
			980					985					990						
Tyr	Asn	Pro	Glu	Val	Glu	Lys	Arg	Asn	Gln	Thr	Val	Asp	Thr	Thr	Asn				
		995					1000					1005							
Ile	Thr	Thr	Pro	Asn	Asp	Ile	Gln	Ala	Asp	Ala	Pro	Ser	Ala	Gln	Ser				
	1010					1015					1020								
Asn	Asn	Glu	Glu	Ile	Ala	Arg	Val	Glu	Thr	Pro	Val	Pro	Pro	Pro	Ala				
1025				1030						1035					1040				
Pro	Ala	Thr	Glu	Ser	Ala	Ile	Ala	Ser	Glu	Gln	Pro	Glu	Thr	Arg	Pro				
				1045					1050					1055					
Ala	Glu	Thr	Ala	Gln	Pro	Ala	Met	Glu	Glu	Thr	Asn	Thr	Ala	Asn	Ser				
			1060					1065					1070						
Thr	Glu	Thr	Ala	Pro	Lys	Ser	Asp	Thr	Ala	Thr	Gln	Thr	Glu	Asn	Pro				
	1075					1080						1085							
Asn	Ser	Glu	Ser	Val	Pro	Ser	Glu	Thr	Thr	Glu	Lys	Val	Ala	Glu	Asn				
	1090					1095					1100								
Pro	Pro	Gln	Glu	Asn	Glu	Thr	Val	Ala	Lys	Asn	Glu	Gln	Glu	Ala	Thr				
1105				1110						1115				1120					
Glu	Pro	Thr	Pro	Gln	Asn	Gly	Glu	Val	Ala	Lys	Glu	Asp	Gln	Pro	Thr				
			1125						1130				1135						
Val	Glu	Ala	Asn	Thr	Gln	Thr	Asn	Glu	Ala	Thr	Gln	Ser	Glu	Gly	Lys				
			1140					1145					1150						
Thr	Glu	Glu	Thr	Gln	Thr	Ala	Glu	Thr	Lys	Ser	Glu	Pro	Thr	Glu	Ser				
	1155						1160					1165							
Val	Thr	Val	Ser	Glu	Asn	Gln	Pro	Glu	Lys	Thr	Val	Ser	Gln	Ser	Thr				
	1170					1175					1180								
Glu	Asp	Lys	Val	Val	Val	Glu	Lys	Glu	Glu	Lys	Ala	Lys	Val	Glu	Thr				
1185				1190						1195				1200					
Glu	Glu	Thr	Gln	Lys	Ala	Pro	Gln	Val	Thr	Ser	Lys	Glu	Pro	Pro	Lys				
			1205						1210				1215						
Gln	Ala	Glu	Pro	Ala	Pro	Glu	Glu	Val	Pro	Thr	Asp	Thr	Asn	Ala	Glu				
			1220					1225					1230						
Glu	Ala	Gln	Ala	Leu	Gln	Gln	Thr	Gln	Pro	Thr	Thr	Val	Ala	Ala	Ala				
	1235					1240						1245							
Glu	Thr	Thr	Ser	Pro	Asn	Ser	Lys	Pro	Ala	Glu	Glu	Thr	Gln	Gln	Pro				
	1250					1255					1260								

Ser Glu Lys Thr Asn Ala Glu Pro Val Thr Pro Val Val Ser Glu Asn
 1265 1270 1275 1280
 Thr Ala Thr Gln Pro Thr Glu Thr Glu Glu Thr Ala Lys Val Glu Lys
 1285 1290 1295
 Glu Lys Thr Gln Glu Val Pro Gln Val Ala Ser Gln Glu Ser Pro Lys
 1300 1305 1310
 Gln Glu Gln Pro Ala Ala Lys Pro Gln Ala Gln Thr Lys Pro Gln Ala
 1315 1320 1325
 Glu Pro Ala Arg Glu Asn Val Leu Thr Thr Lys Asn Val Gly Glu Pro
 1330 1335 1340
 Gln Pro Gln Ala Gln Pro Gln Thr Gln Ser Thr Ala Val Pro Thr Thr
 1345 1350 1355 1360
 Gly Glu Thr Ala Ala Asn Ser Lys Pro Ala Ala Lys Pro Gln Ala Gln
 1365 1370 1375
 Ala Lys Pro Gln Thr Glu Pro Ala Arg Glu Asn Val Ser Thr Val Asn
 1380 1385 1390
 Thr Lys Glu Pro Gln Ser Gln Thr Ser Ala Thr Val Ser Thr Glu Gln
 1395 1400 1405
 Pro Ala Lys Glu Thr Ser Ser Asn Val Glu Gln Pro Ala Pro Glu Asn
 1410 1415 1420
 Ser Ile Asn Thr Gly Ser Ala Thr Thr Met Thr Glu Thr Ala Glu Lys
 1425 1430 1435 1440
 Ser Asp Lys Pro Gln Met Glu Thr Val Thr Glu Asn Asp Arg Gln Pro
 1445 1450 1455
 Glu Ala Asn Thr Val Ala Asp Asn Ser Val Ala Asn Asn Ser Glu Ser
 1460 1465 1470
 Ser Glu Ser Lys Ser Arg Arg Arg Arg Ser Val Ser Gln Pro Lys Glu
 1475 1480 1485
 Thr Ser Ala Glu Glu Thr Thr Val Ala Ser Thr Gln Glu Thr Thr Val
 1490 1495 1500
 Asp Asn Ser Val Ser Thr Pro Lys Pro Arg Ser Arg Arg Thr Arg Arg
 1505 1510 1515 1520
 Ser Val Gln Thr Asn Ser Tyr Glu Pro Val Glu Leu Pro Thr Glu Asn
 1525 1530 1535
 Ala Glu Asn Ala Glu Asn Val Gln Ser Gly Asn Asn Val Ala Asn Ser
 1540 1545 1550
 Gln Pro Ala Leu Arg Asn Leu Thr Ser Lys Asn Thr Asn Ala Val Ile
 1555 1560 1565
 Ser Asn Ala Met Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly Lys
 1570 1575 1580
 Ala Val Ser Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly Gln
 1585 1590 1595 1600
 Tyr Asn Val Trp Ile Ser Asn Thr Ser Met Asn Lys Asn Tyr Ser Ser
 1605 1610 1615
 Glu Gln Tyr Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu Gly

1620	1625	1630
Trp Asp Gln Thr Ile Ser Asn	Asn Val Gln Leu Gly	Gly Val Phe Thr
1635	1640	1645
Tyr Val Arg Asn Ser Asn	Asn Phe Asp Lys Ala	Ser Ser Lys Asn Thr
1650	1655	1660
Leu Ala Gln Val Asn Phe Tyr	Ser Lys Tyr Tyr Ala Asp	Asn His Trp
1665	1670	1675
Tyr Leu Gly Ile Asp Leu Gly	Tyr Gly Lys Phe Gln Ser	Asn Leu Gln
1685	1690	1695
Thr Asn Asn Asn Ala Lys Phe	Ala Arg His Thr Ala Gln	Ile Gly Leu
1700	1705	1710
Thr Ala Gly Lys Ala Phe Asn	Leu Gly Asn Phe Ala Val	Lys Pro Thr
1715	1720	1725
Val Gly Val Arg Tyr Ser Tyr	Leu Ser Asn Ala Asp Phe	Ala Leu Ala
1730	1735	1740
Gln Asp Arg Ile Lys Val Asn	Pro Ile Ser Val Lys Thr	Ala Phe Ala
1745	1750	1755
Gln Val Asp Leu Ser Tyr Thr	Tyr His Leu Gly Glu Phe	Ser Ile Thr
1765	1770	1775
Pro Ile Leu Ser Ala Arg Tyr	Asp Ala Asn Gln Gly Asn	Gly Lys Ile
1780	1785	1790
Asn Val Ser Val Tyr Asp Phe	Ala Tyr Asn Val Glu Asn	Gln Gln Gln
1795	1800	1805
Tyr Asn Ala Gly Leu Lys Leu	Lys Tyr His Asn Val Lys	Leu Ser Leu
1810	1815	1820
Ile Gly Gly Leu Thr Lys Ala	Lys Gln Ala Glu Lys Gln	Lys Thr Ala
1825	1830	1835
Glu Val Lys Leu Ser Phe Ser	Phe	
1845		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Asp Ser Gly Ser Pro Met Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asp Ser Gly Ser Pro Leu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Thr Tyr Phe Gly Ile Asp
1 5